

Substitute_Sequence_Listing_CRF.txt
SEQUENCE LISTING

<110> ZENSUN(SHANGHAI)SCIENCE AND TECHNOLOGY LIMITED
Zhou, Mingdong

<120> ERBB3 BASED METHODS AND COMPOSITIONS FOR
TREATING NEOPLASMS

<130> 11748-006-999

<140> 10/516,759

<141> 2004-12-02

<150> PCT/CN03/00217

<151> 2003-03-26

<150> CH 02116259

<151> 2002-03-26

<160> 17

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 1342

<212> PRT

<213> Homo sapiens

<400> 1

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Ala	Arg	Gly	Ser	Glu	Val	Gly	Asn	Ser	Gln	Ala	Val	Cys	Pro	Gly	Thr
			20					25					30		
Leu	Asn	Gly	Leu	Ser	Val	Thr	Gly	Asp	Ala	Glu	Asn	Gln	Tyr	Gln	Thr
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Leu	Tyr	Lys	Leu	Tyr	Glu	Arg	Cys	Glu	Val	Val	Met	Gly	Asn	Leu	Glu
	50					55					60				
Ile	Val	Leu	Thr	Gly	His	Asn	Ala	Asp	Leu	Ser	Phe	Leu	Gln	Trp	Ile
65				70					75					80	
Arg	Glu	Val	Thr	Gly	Tyr	Val	Leu	Val	Ala	Met	Asn	Glu	Phe	Ser	Thr
			85						90					95	
Leu	Pro	Leu	Pro	Asn	Leu	Arg	Val	Val	Arg	Gly	Thr	Gln	Val	Tyr	Asp
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Gly	Lys	Phe	Ala	Ile	Phe	Val	Met	Leu	Asn	Tyr	Asn	Thr	Asn	Ser	Ser
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His	Ala	Leu	Arg	Gln	Leu	Arg	Leu	Thr	Gln	Leu	Thr	Glu	Ile	Leu	Ser
	130					135					140				
Gly	Gly	Val	Tyr	Ile	Glu	Lys	Asn	Asp	Lys	Leu	Cys	His	Met	Asp	Thr
145					150					155				160	
Ile	Asp	Trp	Arg	Asp	Ile	Val	Arg	Asp	Arg	Asp	Ala	Glu	Ile	Val	Val
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Lys	Asp	Asn	Gly	Arg	Ser	Cys	Pro	Pro	Cys	His	Glu	Val	Cys	Lys	Gly
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Gln	Cys	Cys	His	Asp	Glu	Cys	Ala	Gly	Gly	Cys	Ser	Gly	Pro	Gln	Asp
225					230					235				240	
Thr	Asp	Cys	Phe	Ala	Cys	Arg	His	Phe	Asn	Asp	Ser	Gly	Ala	Cys	Val
			245						250					255	
Pro	Arg	Cys	Pro	Gln	Pro	Leu	Val	Tyr	Asn	Lys	Leu	Thr	Phe	Gln	Leu
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Cys	Pro	Pro	Asp	Lys	Met	Glu	Val	Asp	Lys	Asn	Gly	Leu	Lys	Met	Cys
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Glu	Pro	Cys	Gly	Gly	Leu	Cys	Pro	Lys	Ala	Cys	Glu	Gly	Thr	Gly	Ser
			325						330					335	
Gly	Ser	Arg	Phe	Gln	Thr	Val	Asp	Ser	Ser	Asn	Ile	Asp	Gly	Phe	Val
			340					345					350		
Asn	Cys	Thr	Lys	Ile	Leu	Gly	Asn	Leu	Asp	Phe	Leu	Ile	Thr	Gly	Leu
		355					360					365			
Asn	Gly	Asp	Pro	Trp	His	Lys	Ile	Pro	Ala	Leu	Asp	Pro	Glu	Lys	Leu
	370					375					380				
Asn	Val	Phe	Arg	Thr	Val	Arg	Glu	Ile	Thr	Gly	Tyr	Leu	Asn	Ile	Gln
385					390					395					400
Ser	Trp	Pro	Pro	His	Met	His	Asn	Phe	Ser	Val	Phe	Ser	Asn	Leu	Thr
				405					410					415	
Thr	Ile	Gly	Gly	Arg	Ser	Leu	Tyr	Asn	Arg	Gly	Phe	Ser	Leu	Leu	Ile
			420					425					430		
Met	Lys	Asn	Leu	Asn	Val	Thr	Ser	Leu	Gly	Phe	Arg	Ser	Leu	Lys	Glu
		435					440					445			
Ile	Ser	Ala	Gly	Arg	Ile	Tyr	Ile	Ser	Ala	Asn	Arg	Gln	Leu	Cys	Tyr
	450					455					460				
His	His	Ser	Leu	Asn	Trp	Thr	Lys	Val	Leu	Arg	Gly	Pro	Thr	Glu	Glu
465					470					475					480
Arg	Leu	Asp	Ile	Lys	His	Asn	Arg	Pro	Arg	Arg	Asp	Cys	Val	Ala	Glu
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Gly	Lys	Val	Cys	Asp	Pro	Leu	Cys	Ser	Ser	Gly	Gly	Cys	Trp	Gly	Pro
			500					505					510		
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		515					520					525			
Cys	Val	Thr	His	Cys	Asn	Phe	Leu	Asn	Gly	Glu	Pro	Arg	Glu	Phe	Ala
	530					535					540				
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Gly	Thr	Ala	Thr	Cys	Asn	Gly	Ser	Gly	Ser	Asp	Thr	Cys	Ala	Gln	Cys
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Ala	His	Phe	Arg	Asp	Gly	Pro	His	Cys	Val	Ser	Ser	Cys	Pro	His	Gly
			580					585					590		
Val	Leu	Gly	Ala	Lys	Gly	Pro	Ile	Tyr	Lys	Tyr	Pro	Asp	Val	Gln	Asn
		595					600					605			
Glu	Cys	Arg	Pro	Cys	His	Glu	Asn	Cys	Thr	Gln	Gly	Cys	Lys	Gly	Pro
	610					615					620				
Glu	Leu	Gln	Asp	Cys	Leu	Gly	Gln	Thr	Leu	Val	Leu	Ile	Gly	Lys	Thr
625					630					635					640
His	Leu	Thr	Met	Ala	Leu	Thr	Val	Ile	Ala	Gly	Leu	Val	Val	Ile	Phe
				645					650					655	
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		660					665					670			
Asn	Lys	Arg	Ala	Met	Arg	Arg	Tyr	Leu	Glu	Arg	Gly	Glu	Ser	Ile	Glu
		675					680					685			
Pro	Leu	Asp	Pro	Ser	Glu	Lys	Ala	Asn	Lys	Val	Leu	Ala	Arg	Ile	Phe
	690					695					700				
Lys	Glu	Thr	Glu	Leu	Arg	Lys	Leu	Lys	Val	Leu	Gly	Ser	Gly	Val	Phe
705					710					715					720
Gly	Thr	Val	His	Lys	Gly	Val	Trp	Ile	Pro	Glu	Gly	Glu	Ser	Ile	Lys
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			740					745					750		
Phe	Gln	Ala	Val	Thr	Asp	His	Met	Leu	Ala	Ile	Gly	Ser	Leu	Asp	His
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Ala	His	Ile	Val	Arg	Leu	Leu	Gly	Leu	Cys	Pro	Gly	Ser	Ser	Leu	Gln

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770	Leu	Val	Thr	Gln	Tyr	Leu	Pro	Leu	Gly	Ser	Leu	Leu	Asp	His	Val	Arg
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				805	Gly	Met	Tyr	Tyr	Leu	Glu	Glu	His	Gly	Met	Val	His
			820	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			835	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			850	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			865	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			885	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			900	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			915	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			930	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			945	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			965	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			980	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			995	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1010	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1025	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1045	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1060	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1075	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1090	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1105	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1125	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1140	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1155	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1170	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1185	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1205	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1220	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1235	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
			1250	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
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Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg Ala Phe Gln
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 Gly Pro Gly His Gln Ala Pro His Val His Tyr Ala Arg Leu Lys Thr
 1300 1305 1310
 Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala Phe Asp Asn Pro Asp Tyr
 1315 1320 1325
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 1330 1335 1340

<210> 2
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
 50 55 60
 Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
 65 70 75 80
 Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
 85 90 95
 Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
 100 105 110
 Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
 115 120 125
 His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
 130 135 140
 Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
 145 150 155 160
 Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
 165 170 175
 Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
 180 185 190
 Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
 195 200 205
 Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
 210 215 220
 Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
 225 230 235 240
 Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
 245 250 255
 Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
 260 265 270
 Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
 275 280 285
 Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
 290 295 300
 Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
 305 310 315 320
 Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser
 325 330 335
 Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val
 340 345 350
 Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
 355 360 365
 Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu

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370	Asn	Val	Phe	Arg	Thr	Val	375	Arg	Glu	Ile	Thr	Gly	380	Tyr	Leu	Asn	Ile	Gln
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				405	Arg	Ser	Leu	Tyr	Asn	Arg	Gly	Phe	Ser	Leu	Leu	Leu	Ile	
	Met	Lys	Asn	Leu	Asn	Val	Thr	Ser	Leu	Gly	Phe	Arg	Ser	Leu	Lys	Glu		
	Ile	Ser	Ala	Gly	Arg	Ile	Tyr	Ile	Ser	Ala	Asn	Arg	Gln	Leu	Cys	Tyr		
	His	His	Ser	Leu	Asn	Trp	Thr	Lys	Val	Leu	Arg	Gly	Pro	Thr	Glu	Glu		
465	Arg	Leu	Asp	Ile	Lys	His	470	Asn	Arg	Pro	Arg	Arg	Asp	Cys	Val	Ala	Glu	
				485	Asp	Pro	Leu	Cys	Ser	Ser	Gly	Gly	Cys	Trp	Gly	Pro		
	Gly	Lys	Val	Cys	500				505					510				
	Gly	Pro	Gly	Gln	Cys	Leu	Ser	Cys	Arg	Asn	Tyr	Ser	Arg	Gly	Gly	Val		
	Cys	Val	Thr	His	Cys	Asn	Phe	Leu	Asn	Gly	Glu	Pro	Arg	Glu	Phe	Ala		
	His	Glu	Ala	Glu	Cys	Phe	Ser	Cys	His	Pro	Glu	Cys	Gln	Pro	Met	Glu		
545	Gly	Thr	Ala	Thr	Cys	Asn	Gly	Ser	Gly	Ser	Asp	Thr	Cys	Ala	Gln	Cys		
				565					570									
	Ala	His	Phe	Arg	Asp	Gly	Pro	His	Cys	Val	Ser	Ser	Cys	Pro	His	Gly		
	Val	Leu	Gly	Ala	Lys	Gly	Pro	Ile	Tyr	Lys	Tyr	Pro	Asp	Val	Gln	Asn		
			595					600					605					
	Glu	Cys	Arg	Pro	Cys	His	Glu	Asn	Cys	Thr	Gln	Gly	Cys	Lys	Gly	Pro		
	Glu	Leu	Gln	Asp	Cys	Leu	615	Gln	Thr	Leu	Val	620	Leu	Ile	Gly	Lys	Thr	
625						630					635							

<210> 3
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 <212> PRT
 <213> Homo sapiens

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			20						25					30				
	Leu	Asn	Gly	Leu	Ser	Val	Thr	Gly	Asp	Ala	Glu	Asn	Gln	Tyr	Gln	Thr		
			35					40					45					
	Leu	Tyr	Lys	Leu	Tyr	Glu	Arg	Cys	Glu	Val	Val	Met	Gly	Asn	Leu	Glu		
			50				55					60						
	Ile	Val	Leu	Thr	Gly	His	Asn	Ala	Asp	Leu	Ser	Phe	Leu	Gln	Trp	Ile		
65	Arg	Glu	Val	Thr	Gly	Tyr	Val	Leu	Val	Ala	Met	Asn	Glu	Phe	Ser	Thr		
				85					90									
	Leu	Pro	Leu	Pro	Asn	Leu	Arg	Val	Val	Arg	Gly	Thr	Gln	Val	Tyr	Asp		
			100						105					110				
	Gly	Lys	Phe	Ala	Ile	Phe	Val	Met	Leu	Asn	Tyr	Asn	Thr	Asn	Ser	Ser		
			115					120					125					
	His	Ala	Leu	Arg	Gln	Leu	Arg	Leu	Thr	Gln	Leu	Thr	Glu	Ile	Leu	Ser		
			130				135					140						
	Gly	Gly	Val	Tyr	Ile	Glu	Lys	Asn	Asp	Lys	Leu	Cys	His	Met	Asp	Thr		
145	Ile	Asp	Trp	Arg	Asp	Ile	Val	Arg	Asp	Arg	Asp	Ala	Glu	Ile	Val	Val		
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180 185 190

<210> 4
<211> 1914
<212> DNA
<213> Homo sapiens

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gctgagaacc aataccagac actgtacaag ctctacgaga ggtgtgaggt ggtgatggg 180
aaccttgaga ttgtgctcac gggacacaat gccgacctct ctttcctgca gtggattcga 240
gaagtgcacg gctatgtcct cgtggccatg aatgaattct ctactctacc attgcccaac 300
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aagtaccag atgttcagaa tgaatgtcgg ccctgccatg agaactgcac ccagggggtg 1860
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<211> 475
<212> DNA
<213> Homo sapiens

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tcacgggaca caatgccgac ctctccttcc tgcagtggat tcgagaagt acaggctatg 180
tcctcgtggc catgaatgaa ttctctactc taccattgcc caacctccgc gtggtgagcga 240
ggaccaggt ctacgatggg aagtttgcca tcttcgtcat gttgaactat aacaccaact 300
ccagccacgc tctgcgccag ctccgcttga ctcagctcac cgagattctg tcagggggtg 360
tttatattga gaagaacgat aagctttgtc acatggacac aattgactgg agggacatcg 420
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<400> 6
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<210> 7
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<220>
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<400> 7
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 8
 tttctgcgga gtcacg 16

<210> 9
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 9
 gacgacgacg acaag 15

<210> 10
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 10
 gccatggctg atatcg 16

<210> 11
 <211> 23
 <212> DNA
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<220>
 <223> Primer

<400> 11
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<212> DNA

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<220>

<223> Primer

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<210> 13

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<213> Artificial sequence

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<223> Primer

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<211> 89

<212> PRT

<213> Homo sapiens

<400> 14

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35 40 45
Gly Cys Trp Gly Pro Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr
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<213> Homo sapiens

<400> 15

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<211> 151

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<213> Homo sapiens

<400> 16

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Substitute_Sequence_Listing_CRF.txt

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		35					40					45			
Glu	Gly	Thr	Gly	Ser	Gly	Ser	Arg	Phe	Gln	Thr	Val	Asp	Ser	Ser	Asn
	50					55					60				
Ile	Asp	Gly	Phe	Val	Asn	Cys	Thr	Lys	Ile	Leu	Gly	Asn	Leu	Asp	Phe
65					70				75					80	
Leu	Ile	Thr	Gly	Leu	Asn	Gly	Asp	Pro	Trp	His	Lys	Ile	Pro	Ala	Leu
				85					90					95	
Asp	Pro	Glu	Lys	Leu	Asn	Val	Phe	Arg	Thr	Val	Arg	Glu	Ile	Thr	Gly
			100					105					110		
Tyr	Leu	Asn	Ile	Gln	Ser	Trp	Pro	Pro	His	Met	His	Asn	Phe	Ser	Val
		115					120					125			
Phe	Ser	Asn	Leu	Thr	Thr	Ile	Gly	Gly	Arg	Ser	Lys	Leu	Ala	Ala	Ala
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Leu	Glu	His	His	His	His	His									
145					150										

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